



1600

RAW SEQUENCE LISTING

DATE: 04/23/2003

PATENT APPLICATION: US/09/905,589A

TIME: 13:02:46

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\04232003\I905589A.raw

3 <110> APPLICANT: Chadwick, Brian Paul
 4 Frischauf, Anna Maria
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
 AND NUCLEIC

7 ACIDS
 9 <130> FILE REFERENCE: 28110/36120D
 11 <140> CURRENT APPLICATION NUMBER: 09/905,589A
 12 <141> CURRENT FILING DATE: 2001-07-13
 14 <150> PRIOR APPLICATION NUMBER: 09/240,639
 15 <151> PRIOR FILING DATE: 1999-01-29
 17 <160> NUMBER OF SEQ ID NOS: 32
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2762
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo Sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (232)..(1599)
 29 <223> OTHER INFORMATION:

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37	gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttcaga	180
39	aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga	237
40		Met Arg
41		
43	aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc	285
44	Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
45	5 10 15	
47	ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg	333
48	Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
49	20 25 30	
51	cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc	381
52	His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
53	35 40 45 50	
55	ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct	429
56	Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
57	55 60 65	
59	gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc	477
60	Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
61	70 75 80	
63	act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa	525
64	Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	

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67	act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt			573
68	Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu			
69	100	105	110	
71	tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa			621
72	Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu			
73	115	120	125	130
75	cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc			669
76	Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala			
77	135	140	145	
79	acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga			717
80	Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly			
81	150	155	160	
83	gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca			765
84	Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala			
85	165	170	175	
87	tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca			813
88	Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr			
89	180	185	190	
91	gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc			861
92	Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser			
93	195	200	205	210
95	ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga			909
96	Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly			
97	215	220	225	
99	gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag			957
100	Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln			
101	230	235	240	
103	gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc			1005
104	Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr			
105	245	250	255	
107	tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca			1053
108	Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala			
109	260	265	270	
111	cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga			1101
112	Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly			
113	275	280	285	290
115	aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg			1149
116	Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp			
117	295	300	305	
119	gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca			1197
120	Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala			
121	310	315	320	
123	agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac			1245
124	Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn			
125	325	330	335	
127	aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc			1293
128	Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe			
129	340	345	350	

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132 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
133 355          360          365          370
135 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac      1389
136 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
137          375          380          385
139 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc      1437
140 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
141          390          395          400
143 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc      1485
144 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
145          405          410          415
147 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc      1533
148 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
149          420          425          430
151 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga      1581
152 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
153 435          440          445          450
155 cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag      1629
156 Gln Lys Ser Pro Ala Ser
157          455
159 cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcac ctagaggagcc      1689
161 acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg      1749
163 tgctgccctg gcatcagcct ctccagtcac catctggcca gagggctgtc tggacctggg      1809
165 ccctgtctaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac      1869
167 aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catcccatg cccgtccgc      1929
169 ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca      1989
171 gtttctctcc cagggcagag ctcccttcc tgcaagagtc tgggaggcgg tgcaggctgt      2049
173 cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg      2109
175 cggcaccact gggaactctg gacttgagtg tgtttgctct tccttgggta tgaatgtgtg      2169
177 agttcaccca gaggcctgct ctctcacac attgtgtggt ttggggttaa tgatggaggg      2229
179 agacacctct tcatagacgg caggtgcccc cctttcaggg agtctcccag catgggcgga      2289
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183 gtgtgggtgc caagtgttg tgtagaaaact gtgttctgag ccccttttc tggacaccaa      2409
185 ctgtgtcctg tgaatgtatc gctactgtga gctgttccc cctagccagg gccatgtctt      2469
187 aggtgcagct gtgccacggg tcagctgagc cacagtcccc gaaccaagct ctcggtgtct      2529
189 cgggccacca tccgccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc      2589
191 gggccgtgca tcctgtctag tgtggcgta gtgtcggggc tgagcccctt gagctgtctc      2649
193 agtgaatgta cagtgtcccg cagagctga acctcatgtg ttccactccc aataaaaggt      2709
195 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa      2762
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199 <211> LENGTH: 456
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo Sapiens
203 <400> SEQUENCE: 2
205 Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
206 1          5          10          15
209 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
210          20          25          30

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213 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
214          35          40          45
217 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
218          50          55          60
221 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
222 65          70          75          80
225 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
226          85          90          95
229 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
230          100          105          110
233 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
234          115          120          125
237 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
238          130          135          140
241 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
242 145          150          155          160
245 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
246          165          170          175
249 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
250          180          185          190
253 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
254          195          200          205
257 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
258          210          215          220
261 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
262 225          230          235          240
265 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
266          245          250          255
269 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
270          260          265          270
273 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
274          275          280          285
277 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
278          290          295          300
281 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
282 305          310          315          320
285 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
286          325          330          335
289 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
290          340          345          350
293 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
294          355          360          365
297 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
298          370          375          380
301 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
302 385          390          395          400
305 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
306          405          410          415
309 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val

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310          420          425          430
313 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
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318          450          455
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322 <211> LENGTH: 2797
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo Sapiens
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336          Met Phe Thr Val Leu Thr Arg Gln Pro Cys
337          1          5          10
339 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc      160
340 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
341          15          20          25
343 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc      208
344 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
345          30          35          40
347 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt      256
348 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
349          45          50          55
351 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa      304
352 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
353          60          65          70
355 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc      352
356 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
357 75          80          85          90
359 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc      400
360 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
361          95          100          105
363 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg      448
364 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
365          110          115          120
367 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc      496
368 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
369          125          130          135
371 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat      544
372 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
373          140          145          150
375 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac      592
376 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
377 155          160          165          170
379 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga      640

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\EBONY'S\EP.txt
Output Set: N:\CRF4\04232003\I905589A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

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Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\04232003\I905589A.raw

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L:332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:329
L:664 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:661
L:924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:921